

BASE COUNT 183 a 51 c 90 g 138 t
ORIGIN
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAATGGGCGCGCATATCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaudo."
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 386.
Location/Qualifiers
1. 434
/organism="Homo sapiens"
/db_xref="GDB:5587103"
/db_xref="taxon:9606"
/clone="INAGE:683763"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Altman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAATGGGCGCGCATATCTTTTTTTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaudo."

Query Match 33.2%; Score 429.6; DB 9; Length 462;
Best Local Similarity 98.7%; Pred. No. 1.7e-37; Indels 2; Gaps 2;
Matches 434; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
806 ctgaaattccctgggtctgtccattttgagcgaattggccttgggaaacacggtt 865
|||||
462 CTGAATATCCCTGGTCTCTTCATTTTGAGCGAATTTGGCCTTGGGAAACACGTT 403
866 ctcccttcgattcttcacccggttcacggtatgaatttcctcccaaatatagatct 925
|||||
402 CTTCCTTTCCGATTTCTCATCCGCTCTAC-GCTATGCAATTTCTCCCAATATAGATCT 344
926 tattctgcattctccctactattataatcacacacacactactatttcttcttc 985
|||||
343 TATTTCGTCATTTCCCTCTCTTAAATACACCAACACTTACTATTTCTTATC 284
986 tcttcaactttttaaataatcttccaccaggttatatttgggtattttt-ttccaaacat 1044
|||||
283 TCCTTCACTTTTAAATATCTTTTACCAGGTATACCTTGGTATATTCTTCCAAACAT 224
1045 ttttaagcactgaatcgaacagcctcaaatgaaatgaatgcattgttttggat 1104
|||||
223 TTTTAAAGCACTGAATATCGAACAAGCACTCAAAATGAAGTATCATGTTTGTGTAT 164
1105 ttttcgctgataaaattatttaacatttatatttttacttgattgattgacatgta 1164
|||||
163 TTTTCGCTGATAAAATATTATTAACATTTATTTTACTTGATTCATATGACATGTA 104
1165 tgaattgtaaaataactaatattcaactaatatattgataaataatgattgattgatt 1224
|||||
103 TGTAAATGTAATAATCTAATATTCACATATATATGATATGATCAATGATTTGTTAACT 44
1225 tctttatgtaagtatggtatataaaatttcaagacgaaaa 1264
|||||
43 TCTTTTATGTAAGTATGATATATAAAATTTCAAGACGAACA 4

RESULT 11
AA227632/C 434 bp mRNA linear EST 13-AUG-1997
LOCUS zr98h02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683763 5' similar to TR:G349315 G349315 SYNTAXIN 2'', ;, mRNA sequence.
ACCESSION AA227632
VERSION AA227632.1 GI:1849203
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 434)
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
TITLE Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand

Query Match 32.5%; Score 421.4; DB 9; Length 434;
Best Local Similarity 99.5%; Pred. No. 1.3e-36;
Matches 433; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 172 gagagcgcattccgcagctacacagctcttcttgcagatggcggtctggtgagaag 231
|||||
Db 434 GAGAGCCCCATCCGCGAGGTACACGAGCTCTCTTTCAGATGGCGGTGCTGGTGAGAG 375
232 caggccgacacccctgaacgtcatcgactcaacgtacaaaagacggtcgactacacccgc 291
|||||
Db 374 CAGCGCGACACCCCTGAAGTCTATCGAGTCAACGCTACAAAGACGCTGACTACACCGC 315
292 caggccaaaggcgcgggctgaggaagccgctgagtcagtcaggaagaacccctgcgggacc 351
|||||
Db 314 CAGCCCAAGGCGCAGGTGCGGAAGCCGCTGCAGTACGAGAGAGAGAACCCCTGCCGGACC 255
352 ctctgctgcttctctgctccctgctcaagtagcagcgcgcgcgcgcgcgcgcgcgcgc 411
|||||
Db 254 CTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 195
412 tccagagaccatggagcgcgctgggaagacgctcaccacaaagccggagctctgcccctgag 471
|||||
Db 194 TCCGAGACCATGGAGCGGCTGGGAAGGACG-CACCAAAAGCCGGAGGCTCTGCCCTGCAG 136
472 ggagttgcccccaaccccttccggaactcagttcttagaaaaagaacgcccaggttcaagaa 531
|||||
Db 135 GGAGTTGCCCAACCCCTTCCGGAATCAGTCTTTAGAAAAGAAACGCGCAGGTTCAAGAA 76
532 ttgcaaacaccgctgctgtggaagatggttagttgataccgctccgattcttctcagt 591
|||||
Db 75 TTGCAAAACAGCCTGCTGCTGGAAAGATGGTGTAGTTGATACCGTCCGATGATTTCTCAGT 16
592 aaagatagattccca 606
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Db 15 AAAGATAGATCCCA 1
RESULT 12
AW500047
LOCUS
DEFINITION UI-HF-BNO-ak1-a-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077288 5', mRNA sequence.
ACCESSION AW500047
VERSION AW500047.1 GI:7112287
KEYWORDS EST.

1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library.
BASE COUNT 182 a 203 c 216 g 138 t
ORIGIN

Query Match 56.2%; Score 728; DB 10; Length 739;
Best Local Similarity 99.9%; Pred. No. 1.4e-65;
Matches 739; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 29 aggaagtctcgggaccagatcagagacatgttcgagcagggtaagtggagcgtgtttt 88
Db 1 AGGAAGTCTCGGGACACAGATCAGGACATGTTCCGAGCAGGGTAAGTGGGACGTGTTT 60
QY 89 ccgagaactctgctgcgcagcgtgaagggcgcgccgcccctcaacagagatcagagacc 148
-- 61 CCGAGAACTTGTCTGGCGACGTGAAGGGCGCGCGCGCCCTCAACGAGATCGAGAGCC 120
149 gccaccgcgaactctgctgcgcagcgcgcacatccgcagctacagagctcttcttgc 208
Db 121 GCCACCGCAACTGCTCGGCTGGAGAGCCGATCCGCGAGCTACAGAGCTCTTCTTGC 180
QY 209 agatggcggtgctggtgagaagcagccgacacccctgaactgcagctcagcgtacacgtac 268
Db 181 AGATGGCGGTGCTGGTGGAGAGCAGCCGACACCTGAAGCTCATCGAGTCAACGTAC 240
QY 269 aaagacgctgactacacccgcccagggccagggcgcaggtgctgctcctcctcaagttagc 328
Db 241 AAAAGAGCGGTGCTGCTACACCGCGGCGAGGCGGAGGCGGAGGCGGCGGCGGCGG 300
QY 329 agagaagaacccctgcgcagcctctgctgtcttctgctcctcctcctcctcctcctcct 388
Db 301 AGAGAGAAACCCCTGCGGACCCCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 389 ccgcccggcgccgacccgcccacccagaccatcccgagcgtgctgggaagcagctcacc 448
Db 361 CCG 419
QY 449 aagccggagctcgtcctcagggagttgcccacaccccttccgggaactcagctcttag 508
Db 420 AAGCCGGAGCTGCTGCGCTCAGGGAGTGTCCCAACCTTCCGGAACCTCAGTCTTAG 479
QY 509 aaagaaacccaggttcaagaattgcaaacacagcctgctgctggaagatggttagttg 568
Db 480 AAAAGAAACCCAGGTTCAAGATTGCAACACCGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
QY 569 ataccgtccgagtgattcttcagtaaatagattcccaacaaagtgtgcaatgtcattat 628
Db 540 ATACCGTCCGATGATCTTTCAGTAAAGATAGATTCCCAACAAAGTTGTGCAATGTCATTAT 599
QY 629 atgacacctgactcttaccgtcttgacgaagcgaagtaaggaactgaagttgtatct 688
Db 600 ATGACACCTTGCACCTCTTACCGCTTTCAGAGAGCCCAAGTAAGGAAGTGTATCT 659
QY 689 gactgaggtgaatgtctgagccctcctcctaataagacactcaaggaaggaagtaatt 748
Db 660 GACTGTAGGTGAATGTCTGAGGCTTCCCTCTTAATAAGACTCAAGGAGGAAGTCAATT 719
QY 749 gggcatctgctaataagaatg 768
Db 720 GGSCATCTGCTAATAAGATG 739

RESULT 2
BI519530/c
LOCUS 603061815T1 NIH_MGC_118 Homo sapiens cdna clone IMAGE:5211074 3',
DEFINITION mRNA sequence.
ACCESSION BI519530
VERSION BI519530.1 GI:15344322
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 911)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cspbs-remail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11529 row: n column: 03
High quality sequence start: 3
High quality sequence stop: 890.

FEATURES
source
1..911
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5211074"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
BASE COUNT 199 a 235 c 243 g 234 t
ORIGIN

Query Match 50.9%; Score 658.6; DB 10; Length 911;
Best Local Similarity 94.8%; Pred. No. 3.6e-62;
Matches 854; Conservative 0; Mismatches 29; Indels 18; Gaps 16;
QY 37 tcggcgaccagatcgaggacatgtt--cgagcagggtaagtgggacgtgttttc--cgag 93
Db 900 TCGGGGACACAGATCGAGACATGTTTCGAGCAAGGGTAAGTGAACGCTGTTTTCACGAG 841
QY 94 aactt-gctggcagctgaaggcgcgcgccg-cctcaacagagatcgagaccgcc 151
Db 840 AACTTCGCTTCCGACGTTAAGGGCGCGCGCGCCCTCAACGAGATCGAGAGCCGCC 781
QY 152 a-cgcgaactgtgcctgagagcgcacatccgcgagctacacgagctctcttgcag 210
Db 780 ATCCGCGAAGTCTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATG 721
QY 211 atggc-ggtgctggtgagaagca-ggcgcacacccctgaacgtcatcgagctcaacgtac 268
Db 720 ATGCTGTGCTGTGGAGAGCATGGCGGACACCTTCAACGTCATCGAGTCAACGTAC 661
QY 269 aaaag-acggtcgaactacaccggc-caggccaagggcgaggt-gcggaagccgctgcagt 325
Db 660 AAAAGTACGTCGACTACCGGCACAGGCCAAGCGCAGGTAGCGGAAGCCCTGTCAGT 601
QY 326 acgaggaagaacccctgcgcgaccctctgctcttctctctctctctctctctcaagtagc 385
Db 600 ACGAGGAGAGAACCCCTGCGGACCTCTGCTGCTCTCTGCTGCTCTCTGCTGCTGCTG 541
QY 386 aggcggcccgggcgccgacacccgcatcccgagcattggagcgctggtggagagcgtca 445
Db 540 AGCG 482

Query Match 9.1%; Score 117.2; DB 1; Length 790;
Best Local Similarity 58.2%; Pred. No. 3e-17;
Matches 206; Conservative 0; Mismatches 148; Indels 0; Gaps 5

	Qy	Dq	Score	DB	Length	Mismatches	Indels	Gaps
1	atccagcgccagctggagatcatggtgcgaagaagtctctggcgaccacgatcgaggacatg	60						
437	ATCCAGAGGCACGTGGAGATCACTGCGCGGACCACGACCATGTGAGGAGTTTGAAGACATG	496						
61	ttcgagcagggttaagtgggacgtgttttcccgagaaacttgctggtcgacgctgaaggccgcg	120						
497	CTGGAGAGTGGAATCCGCCATCTTTGCCCTCTGGGATCATATGGACTCAGCATCTCG	556						
121	cgggcgcctccaacgagatcgagagcgcacacgcgaacctgctgcgcttgagagccgcg	180						
557	AAGCAGGCCCCTCAGTAGATCGACACCGCACAGTGAATCATCAAGTTGGAGAACACG	616						
181	atccgcgacgtacacgagctctcttgacagatggtgctggtggagaacacgagcccac	240						
617	ATCCGGGAGCTACAGGATATCTTCATGGACATGCCATGCTGGTGGAGACGACGGGGAG	676						
241	accctgaacgtcatcgagctcaacgatacaaaagacggtcgactcacacgccggccagc	300						
677	ATGATTGACAGGATCGAGTACAATGTGGAACACCGTGTGGACTACGTGGAGAGGCCGTG	736						
301	gcgcaggtgcggaaggcgtgacgtacgagagagaacacccctgcgcgaccctc	354						
737	TCTGACCAAGAAGCCGCTCAAGTACCAGAGCAAGGCACCGAGGAAGAGATC	790						

RESULT 15
US-08-393-985-1
Sequence 1, Application US/08393985
Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Modulation
of Vesicular Release
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250

APPLICATION NUMBER: 135692/1992
FILING DATE: April 30, 1992
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 870
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-690-457-12

Query Match 9.6%; Score 124.8; DB 1; Length 870;
Best Local Similarity 60.7%; Pred. No. 6.3e-19;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;
Qy 1 atccagcgcagctggagatcatggcgaaggaagtctcggcgaccagatcgagacatg 60
|||||
445 ATCCAGCCGAGCTGGAGATCACTGGGAGGACCACTGACGAGGCTGGAAGAGATG 504
Qy 61 ttcagcaggttaagtggagctgtttccgagaaacttgcggcgacgtgaaggcgcg 120
|||||
Db 505 CTGGAGACGGGAAGCCCTCCATCTTCATCTCGGATATATATCAAGATCAAAATCACT 564
Qy 121 cgggcccctcaacgagatcgagagccgaccgcgacgtcgcgcctggagagccgc 180
|||||
Db 565 AGGCAAGCTCTCATGATGATCGAGTCCGCCACCAAGACATCAGTGGAGACCAAGC 624
Qy 181 atccgcagctacagagctcttcttcagatggcggtgctggagaaagcagccgc 240
|||||
Db 625 ATCCGAGAGCTGCAGAGATGTTATGATATGGCCATGTTGTCGAGACTCAGGGTGA 684
Qy 241 accctgaagctacagctcaacgtacaaaagcggctcgactacacggcgccagc 300
|||||
Db 685 ATGGTCAACAACATCGAGAGAAATGTGTGAACCTGTAGATTACGTGGAACATGCCAAG 744
Qy 301 gcgcaggtgcggaagccgtgcagtcagagagaag 336
|||||
Db 745 GAAGAGACGAAGAAGCCATCAATACCAGAGCAAG 780
|||||

RESULT 10
US-08-628-187-12
Sequence 12, Application US/08628187
Patent No. 5837239
GENERAL INFORMATION:
APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE DESIGNATED
AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTIBODIES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA, Japan
STREET: 1, Taya-cho
CITY: Yokohama-shi
COUNTRY: Japan
ZIP: 244
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,187
FILING DATE: April 5, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 294856/1991
FILING DATE: October 16, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 294857/1991
FILING DATE: October 16, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122906/1992

FILING DATE: April 17, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 135692/1992
FILING DATE: April 30, 1992
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 870
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-628-187-12

Query Match 9.6%; Score 124.8; DB 2; Length 870;
Best Local Similarity 60.7%; Pred. No. 6.3e-19;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;
Qy 1 atccagcgcagctggagatcatggcgaaggaagtctcggcgaccagatcgagacatg 60
|||||
445 ATCCAGCCGAGCTGGAGATCACTGGGAGGACCACTGACGAGGCTGGAAGAGATG 504
Qy 61 ttcagcaggttaagtggagctgtttccgagaaacttgcggcgacgtgaaggcgcg 120
|||||
Db 505 CTGGAGACGGGAAGCCCTCCATCTTCATCTCGGATATATATCAAGATCAAAATCACT 564
Qy 121 cgggcccctcaacgagatcgagagccgaccgcgacgtcgcgcctggagagccgc 180
|||||
Db 565 AGGCAAGCTCTCAATGAGATCGAGTCCGCCACCAAGACATCAGTGGAGACCAAGC 624
Qy 181 atccgcagctacagagctcttcttcagatggcggtgctggagaaagcagccgc 240
|||||
Db 625 ATCCGAGAGCTGCAGAGATGTTATGATATGGCCATGTTGTCGAGACTCAGGGTGA 684
Qy 241 accctgaagctacagctcaacgtacaaaagcggctcgactacacggcgccagc 300
|||||
Db 685 ATGGTCAACAACATCGAGAGAAATGTGTGAACCTGTAGATTACGTGGAACATGCCAAG 744
Qy 301 gcgcaggtgcggaagccgtgcagtcagagagaag 336
|||||
Db 745 GAAGAGACGAAGAAGCCATCAATACCAGAGCAAG 780
|||||

RESULT 11
US-08-690-457-15
Sequence 15, Application US/08690457
Patent No. 5726298
GENERAL INFORMATION:
APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE
DESIGNATED AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTI
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA,
STREET: 1, Taya-cho
CITY: Yokohama-shi
COUNTRY: Japan
ZIP: 244
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,457
FILING DATE: 16-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/078,309
FILING DATE: June 15, 1993
APPLICATION NUMBER: 294856/1991

QY 1 atccagcgcagctgagatcattggaagaaagtcctcgccgaccagatcgaggacatg 60
 Db 445 ATCCAGCGCCAGCTGGAGATCATTGGAGAGACCACCACTGACGACGAGCTGGAGAGATG 504
 QY 61 ttcgagcaggtgaagtggagcgtgttttcgagaaacttgcctgcccagcgtgaaggcgcg 120
 Db 505 CTGGAGAGCGGGAAGCGCTCCTTCATCTCGGATATTATATCAGATTACAAATCACT 564
 QY 121 cgggcgcctcaacgagatcgagagccgaccgcggaactgctgcgctggagagccgc 180
 Db 565 AGCAAGCTCTCAATGAGATCGAGTCCCGCCACAAGACATCATGAACTGGAGACGAGC 624
 QY 181 atccgcagctacacagctcttcttcagatgctgctggtggagaaagcagggcgac 240
 Db 625 ATCCGAGAGCTGACGAGATGTTTCATGGATATGGCCATGTTTGTGAGACTCAGGGTGAA 684
 QY 241 acctgaacgtcatcagctcagctacaaagacggtgcactacacggccagggccaaag 300
 Db 685 ATGGTCAACAACATCGAGAGAAATGTGTGAACCTCTGTAGATTACGTGGAACATGCCAAG 744
 QY 301 ggcaggtgcggaagcgcgtgagtcagagagaag 336
 Db 745 GAAGAGACGAAGAAGCCATCAATACCGAGAGCAAG 780

RESULT 6
 US-08-628-187-14
 ; Sequence 14, Application US/08628187
 ; Patent No. 5837239
 ; GENERAL INFORMATION:
 ; APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.
 ; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE DESIGNATED
 ; TITLE OF INVENTION: AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTIBODIES THEREO
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA, Japan
 ; STREET: 1, Taya-cho
 ; CITY: Yokohama-shi
 ; COUNTRY: Japan
 ; ZIP: 244
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/628,187
 ; FILING DATE: April 5, 1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 294856/1991
 ; FILING DATE: October 16, 1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 294857/1991
 ; FILING DATE: October 16, 1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 122906/1992
 ; FILING DATE: April 17, 1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 135692/1992
 ; FILING DATE: April 30, 1992
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 840
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 US-08-628-187-14

Query Match 9.6%; Score 124.8; DB 2; Length 840;
 Best Local Similarity 60.7%; Pred. No. 6.2e-19;

Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0:
 QY 1 atccagcgcagctgagatcattggaagaaagtcctcgccgaccagatcgaggacatg 60
 Db 445 ATCCAGCGCCAGCTGGAGATCATTGGAGAGACCACCACTGACGACGAGCTGGAGAGATG 504
 QY 61 ttcgagcaggtgaagtggagcgtgttttcgagaaacttgcctgcccagcgtgaaggcgcg 120
 Db 505 CTGGAGAGCGGGAAGCGCTCCTTCATCTCGGATATTATATCAGATTACAAATCACT 564
 QY 121 cgggcgcctcaacgagatcgagagccgaccgcggaactgctgcgctggagagccgc 180
 Db 565 AGCAAGCTCTCAATGAGATCGAGTCCCGCCACAAGACATCATGAACTGGAGACGAGC 624
 QY 181 atccgcagctacacagctcttcttcagatgctgctggtggagaaagcagggcgac 240
 Db 625 ATCCGAGAGCTGACGAGATGTTTCATGGATATGGCCATGTTTGTGAGACTCAGGGTGAA 684
 QY 241 acctgaacgtcatcagctcagctacaaagacggtgcactacacggccagggccaaag 300
 Db 685 ATGGTCAACAACATCGAGAGAAATGTGTGAACCTCTGTAGATTACGTGGAACATGCCAAG 744
 QY 301 ggcaggtgcggaagcgcgtgagtcagagagaag 336
 Db 745 GAGAGACGAAGAAGCCATCAATACCGAGAGCAAG 780

RESULT 7
 US-08-690-457-13
 ; Sequence 13, Application US/08690457
 ; Patent No. 5726298
 ; GENERAL INFORMATION:
 ; APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.
 ; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE
 ; TITLE OF INVENTION: DESIGNATED AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTI
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA,
 ; STREET: 1, Taya-cho
 ; CITY: Yokohama-shi
 ; COUNTRY: Japan
 ; ZIP: 244
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/690,457
 ; FILING DATE: 16-AUG-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/078,309
 ; FILING DATE: June 15, 1993
 ; APPLICATION NUMBER: 294856/1991
 ; FILING DATE: October 16, 1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 294857/1991
 ; FILING DATE: October 16, 1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 122906/1992
 ; FILING DATE: April 17, 1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 135692/1992
 ; FILING DATE: April 30, 1992
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 867
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear

[illegible]

RESULT

US-08-493-071-11
Sequence 11, Application US/08493071
Patent No. 6127149
GENERAL INFORMATION:
APPLICANT: Hirai, Yohei
APPLICANT: Koshida, Shogo
APPLICANT: Oka, Yumiko
TITLE OF INVENTION: MODIFIED EPIMORPHIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 CANAL CENTER PLAZA, SUITE 300
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/493,071
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 715-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-493-071-11

Query Match 9.6%; Score 124.8; DB 3; Length 711;
Best Local Similarity 60.7%; Pred. NO. 5.8e-19;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

[illegible]

Db 685 atgtcaacaacatcgagagaatgtgtgaactctgtagattacgtggacaatgccaa 744

Qy 301 gcgcaggtcgcaagcccgctgcagctacgaggagaag 336
 ||| ||| ||| ||| ||| ||| ||| |||

Db 745 gaagagcagcaagaagcccatcaataaccagagcaag 780
 ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13

AAQ75248
 ID AAQ75248 standard; cDNA; 867 BP.
 XX
 AC AAQ75248;
 XX
 DT 10-AUG-1995 (first entry)
 XX
 DE Mouse epimorphine isoform A gene.
 XX
 KW Probe; epimorphine; human; mouse; lambda-gtl1; expression library;
 KW monoclonal antibody; isoform; drug; congenital; acquired; E.coli;
 KW epidermal abnormality; ds.
 XX
 OS Mus musculus.
 XX

Key	Location/Qualifiers
FT variation	793..867
FT	/*tag= a
FT	/note= "sequence variance in isoform A"

XX JP06293800-A.
 PN
 PD 21-OCT-1994.
 XX
 PF 15-OCT-1992; 92JP-0301581.
 XX
 PR 15-OCT-1992; 92JP-0301581.
 XX
 FA (BIOM-) BIOMATERIAL KENKYUSHO KK.
 XX
 DR WPI; 1995-009638/02.
 DR P-PSDB; AAR66480.
 XX

Human or murine epimorphine - useful for development of drugs to treat congenital and acquired epidermal form abnormality

XX Claim 10; Page 8; 41pp; Japanese.

XX The sequence of the gene encoding mouse epimorphine isoform A. A DNA fragment (AAQ75250) containing the mouse epimorphine gene (AAQ75247) was isolated from a lambda-gtl1 expression cDNA library screened with a monoclonal antibody raised against mouse epimorphine. A probe (AAQ75243) derived from the mouse gene sequence was used to isolate isoforms of the mouse gene (AAQ75248-9) and the gene encoding human epimorphine (AAQ75244) and isoforms (AAQ75245-6). The genes were cloned into expression systems for the production of the protein in E.coli and in animal cells. The epimorphine can be used in the development of drugs to treat both congenital and acquired epidermal form abnormality.

XX Sequence 867 BP; 261 A; 192 C; 245 G; 169 T; 0 other;

Query Match	9.6%	Score 124.8;	DB 16;	Length 867;
Best Local Similarity	60.7%;	Pred. NO. 4.3e-13;		
Matches 204;	Conservative	0;	Mismatches 132;	Indels 0; Gaps

Qy 1 atccagcgccactggagatcatgggcaaggaagtctcgggcgaccagatcgaggacatg 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 445 atccagcgccactggagatcactggaggaccaccactgacgacgactgggaagatg 504
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 ttcgagcagggtaagtggacatgttttcgagaacttgcgtccgacgtgaaggcgcg 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 505 ctggagagcggaagcgtccatcttcactctcggtatttatcatcagattcaccaatcact 564
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 121 cgggcgcgcctcaacagagatcagagccgacccgcaactgctgcgcctggagagcgcg 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

XX New polypeptides contain a first portion of 5-99 amino acids joined
CC to a second portion contg. at least a functional domain of
CC epimorphin. The first portion may be selected from the peptides
CC given in AAR92029 to AAR92036. The second portion may be full-length
CC epimorphin (see AAR92037 to AAR92042 for human and mouse epimorphins).
CC Fragments (123), (2M), (3M) and (23) of epimorphin given in AAT16083
CC to AAT16090 are used in the prodn. of modified epimorphins.
CC 123: N-terminus to right before C-terminal hydrophobic domain.
CC 2M: amino acid 30 to right before C-terminal hydrophobic domain.
CC 3M: amino acid 79 to right before C-terminal hydrophobic domain.
CC 23: amino acid 105 to right before C-terminal hydrophobic domain.
CC The modified epimorphins are useful for the development of diagnosis
CC and treatment of morphogenetic abnormalities of epithelial tissue or
CC novel remedies for wounds, eg burns, after surgery and for artificial
CC organs. They may also be used as components of cosmetics, hair
CC growth stimulators, etc.
XX Sequence 798 BP; 251 A; 177 C; 230 G; 140 T; 0 other;

Query Match          9.6%; Score 124.8; DB 17; Length 798;
Best Local Similarity 60.7%; Pred. No. 4.3e-13;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 atccagcgccagctgagatcattggcgaaggagtcgtcgccgaccagatcgaggacatg 60
   |||||
Db 445 atccagcgccagctgagatcattggcgaaggagtcgtcgccgaccagatcgaggacatg 504

QY 61 ttcgagcagggttaagtggacgtgttttcgcgagaacttgcgtgcgcagctgaaggcgcg 120
   |||||
Db 505 ctggagagcgggaagcgtccattcttcgtcgattatcagattcacaataact 564

QY 121 cgggcgcctcaacagatcgagagcccaacgcgaactcgtcgctgagagccgc 180
   |||||
Db 565 aggcagctctcaatgagatcgatccgcccaagaacatcatgaagctggagaccagc 624

QY 181 atccgcgactacagagctcttcttcgagatggcggtggtgagagcagccgcgac 240
   |||||
Db 625 atccgagactcagagatgttcattgatatggccatgtttgctgagactcagggtgaa 684

QY 241 accctgaactcagatcagctcaacgtacaaaagacggtcgactacaccggccaggccaag 300
   |||||
Db 685 atggtcaacaacatcgagagaaatggtgaaactctgtagattacgtggaacatgccaa 744

QY 301 gcgcaggtgcggaagccgtgcagtcacgagagaag 336
   |||||
Db 745 gaagagacgaagaagccatcaaataccagagcaag 780

RESULT 9
AAT62414
ID AAT62414 standard; cDNA; 798 BP.
XX
XX AAT62414;
XX
XX 02-JUL-1997 (first entry)
XX
XX Mouse epimorphin coding sequence.
XX
XX Human; mouse; epimorphin; coiled-coil region; functional domain; tissue;
XX hydrophobic; deletion; truncation; regulation; morphogenesis; epithelium;
XX artificial organ; cosmetic; hair tonic; ds.
XX
XX Mus musculus.
XX
XX JP09065885-A.
XX
XX 11-MAR-1997.
XX
XX 29-MAR-1996; 96JP-0099684.
XX
XX 19-JUN-1995; 95JP-0175540.

```

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PR 31-MAR-1995; 95JP-0099980.
XX
XX (SUME ) SUMITOMO ELECTRIC IND CO.
XX
XX WPI; 1997-220419/20.
XX
XX Modified epimorphin and related DNA - useful e.g. for treatment of
XX tissues or in artificial organs, or as an ingredient in cosmetics
XX
XX Example 1; Page 14; 18pp; Japanese.
XX
XX The invention relates to novel human (AAW14257-9) or mouse (AAW14260-2)
XX epimorphin proteins with replacements, deletions or substitutions in the
XX amino acid sequence. The new epimorphin protein consists of: (a) an
XX N-terminal coiled-coil region; (b) a functional domain in the middle;
XX and (c) a C-terminal coiled-coil region. A hydrophobic region in the
XX C-terminal has been deleted and at least some amino acids have been
XX deleted from the terminals of coiled coil regions (a) and/or (c). This
XX sequence encodes the complete mouse epimorphin protein. Epimorphin is a
XX protein which regulates morphogenesis of epithelial tissues. It can be
XX used for treatment of tissues or used directly in artificial organs or
XX as an ingredient in cosmetics, hair tonic, etc.
XX
XX Sequence 798 BP; 251 A; 177 C; 230 G; 140 T; 0 other;

Query Match          9.6%; Score 124.8; DB 18; Length 798;
Best Local Similarity 60.7%; Pred. No. 4.3e-13;
Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 1 atccagcgccagctgagatcattggcgaaggagtcgtcgccgaccagatcgaggacatg 60
   |||||
Db 445 atccagcgccagctgagatcattggcgaaggagtcgtcgccgaccagatcgaggacatg 504

QY 61 ttcgagcagggttaagtggacgtgttttcgcgagaacttgcgtgcgcagctgaaggcgcg 120
   |||||
Db 505 ctggagagcgggaagcgtccattcttcgtcgattatcagattcacaataact 564

QY 121 cgggcgcctcaacagatcgagagcccaacgcgaactcgtcgctgagagccgc 180
   |||||
Db 565 aggcagctctcaatgagatcgatccgcccaagaacatcatgaagctggagaccagc 624

QY 181 atccgcgactacagagctcttcttcgagatggcggtggtgagagcagccgcgac 240
   |||||
Db 625 atccgagactcagagatgttcattgatatggccatgtttgctgagactcagggtgaa 684

QY 241 accctgaactcagatcagctcaacgtacaaaagacggtcgactacaccggccaggccaag 300
   |||||
Db 685 atggtcaacaacatcgagagaaatggtgaaactctgtagattacgtggaacatgccaa 744

QY 301 gcgcaggtgcggaagccgtgcagtcacgagagaag 336
   |||||
Db 745 gaagagacgaagaagccatcaaataccagagcaag 780

RESULT 10
AAQ41594
ID AAQ41594 standard; cDNA; 840 BP.
XX
XX AAQ41594;
XX
XX 24-AUG-1993 (first entry)
XX
XX Mouse epimorphin isoform B coding sequence.
XX
XX vascularisation; induction; epithelial tissue morphogenesis; ds.
XX
XX Mus musculus.
XX
XX OS
XX
XX Key Location/Qualifiers
XX 1..840
XX /*tag=
XX /product= epimorphin_isoform_B

```

Db 451 atgtcaacaacatcgagagaaatgtgtgaactctgttagattacgtggaacatgccaaag 510
 Qy 301 gcgcaggtgcggaagccgtgcagtagcagagagaag 336
 Db 511 gaagagacgaagaagccatcaataaccagagcaag 546

RESULT 5
 AAT62412
 ID AAT62412 standard; cDNA; 564 BP.
 XX AC AAT62412;
 XX DT
 XX 02-JUL-1997 (first entry)
 XX Mouse epimorphin truncated variant. 3M coding sequence.
 DE Human; mouse; epimorphin; coiled-coil region; functional domain; tissue;
 KW hydrophobic; deletion; truncation; regulation; morphogenesis; epithelium;
 YV artificial organ; cosmetic; hair tonic; ds.
 XA Synthetic.
 OS JP09065885-A.
 XX PN
 XX 11-MAR-1997.
 PD
 XX 29-MAR-1996; 96JP-0099684.
 XX 19-JUN-1995; 95JP-0175540.
 PR 31-MAR-1995; 95JP-0099980.
 PR
 XX (SUME) SUMITOMO ELECTRIC IND CO.
 PA
 XX WPI; 1997-220419/20.
 DR P-PSDB; AAW14261.
 XX Modified epimorphin and related DNA - useful e.g. for treatment of
 PT tissues or in artificial organs, or as an ingredient in cosmetics
 XX
 PS Example 1; Page 13; 18pp; Japanese.
 XX
 XX The invention relates to novel human (AAW14257-9) or mouse (AAW14260-2)
 CC epimorphin proteins with replacements, deletions or substitutions in the
 CC amino acid sequence. The new epimorphin protein consists of: (a) an
 CC N-terminal coiled-coil region; (b) a functional domain in the middle;
 CC and (c) a C-terminal coiled-coil region. A hydrophobic region in the
 CC C-terminal has been deleted and at least some amino acids have been
 CC deleted from the terminals of coiled coil regions (a) and/or (c). This
 CC sequence encodes the mouse epimorphin protein lacking the N-terminal
 CC 78 amino acids. Epimorphin is a protein which regulates morphogenesis
 CC of epithelial tissues. It can be used for treatment of tissues or used
 CC directly in artificial organs or as an ingredient in cosmetics, hair
 CC tonic, etc.
 XX Sequence 564 BP; 181 A; 124 C; 162 G; 97 T; 0 other;
 SQ

Query Match 9.6%; Score 124.8; DB 18; Length 564;
 Best Local Similarity 60.7%; Pred. No. 4e-13;
 Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 1 atccagccagctggagatcatggcgaagaagtctcggcgaccagatcgaggacatg 60
 Db 211 atccagccagctggagatcatggcgaagaagtctcggcgaccagatcgaggacatg 270
 Qy 61 ttccagcaggtaagtggagctgttttccagaaacttctggcgacgtgaaggcgcg 120
 Db 271 ctgagagcgggagcgctccatctctcgtgatatatcatcagattcacaaatcact 330
 Qy 121 cgggcgcctcaacagatagagagcgccacccgcaactgctgcctggagagcgcg 180
 Db 331 aggcagctctcaatgagatgagctccgcgcacaaagacatcatgaagctggagaccagc 390

Qy 181 atccgcagctacacagagctcttcttcagatggcgggtggtggagaaagcagccgac 240
 Db 391 atccgcagctgcacagagatgttcattgatgcccattgttgcgagactcaggggtgaa 450
 Qy 241 accctgaacgtcatcagctcaacgtacaaaagacggtcgactacacggccagggccaag 300
 Db 451 atggtcaacaacatcgagagaaatgtgtgaactctgttagattacgtggaacatgccaaag 510

Qy 301 gcgcaggtgcggaagccgtgcagtagcagagagaag 336
 Db 511 gaagagacgaagaagccatcaataaccagagcaag 546

RESULT 6
 AAT16086
 ID AAT16086 standard; cDNA; 711 BP.
 XX AC AAT16086;
 XX DT
 XX 30-MAY-1996 (first entry)
 XX Mouse epimorphin fragment (2M).
 DE Mouse epimorphin fragment (2M).
 XX Epimorphin; human; mouse; wound; burn; epithelial tissue;
 KW diagnosis; treatment; morphogenetic abnormality; cosmetic;
 KW hair growth stimulator; ds.
 XX OS Mus musculus.
 XX EP698666-A2.
 XX 28-FEB-1996.
 PD
 XX 20-JUN-1995; 95EP-0304270.
 PF
 XX 31-MAR-1995; 95JP-0099980.
 PR 21-JUN-1994; 94JP-0162874.
 PR 31-MAR-1995; 95JP-0099979.
 XX (SUME) SUMITOMO ELECTRIC IND CO.
 PA
 XX Hirai Y, Koshida S, Oka Y;
 PT WPI; 1996-118213/13.
 DR P-PSDB; AAR92046.
 XX Novel polypeptide containing an epimorphin functional domain - has
 PT possible benefits in epithelial tissue treatments, e.g. burns and
 PT for artificial organs
 XX Claim 27; Page 30; 62pp; English.
 PS
 XX New polypeptides contain a first portion of 5-99 amino acids joined
 CC to a second portion contg. at least a functional domain of
 CC epimorphin. The first portion may be selected from the peptides
 CC given in AAR92029 to AAR92036. The second portion may be full-length
 CC epimorphin (see AAR92037 to AAR92042 for human and mouse epimorphins).
 CC Fragments (123), (2M), (3M) and (23) of epimorphin given in AAT16083
 CC to AAR16090 are used in the prodn. of modified epimorphins.
 CC 123: N-terminus to right before C-terminal hydrophobic domain.
 CC 2M: amino acid 30 to right before C-terminal hydrophobic domain.
 CC 3M: amino acid 79 to right before C-terminal hydrophobic domain.
 CC 23: amino acid 105 to right before C-terminal hydrophobic domain.
 CC The modified epimorphins are useful for the development of diagnosis
 CC and treatment of morphogenetic abnormalities of epithelial tissue or
 CC novel remedies for wounds, eg burns, after surgery and for artificial
 CC organs. They may also be used as components of cosmetics, hair
 CC growth stimulators, etc.
 XX Sequence 711 BP; 232 A; 155 C; 201 G; 123 T; 0 other;
 SQ

PT during apoptosis and/or tumour suppression

PS Claim 1; Page 21; 24pp; French.

XX AA261474-87 represent tumour suppressor activated pathway gene cDNAs, designated TSAP9-TSAP22, respectively. The cellular expression of TSAP genes is induced during apoptosis and tumour suppression. The specification also describes a tumour suppressor inhibited pathway gene TSIP3. Medicaments comprising either vectors for cellular expression of the TSAP genes or TSIP3, proteins encoded by these genes, compounds that ensure cellular expression of these genes, or compounds that inhibit cellular expression of these genes are useful for treating cancer or as antiviral agents. Probes and primers derived from the genes and antigens or antibodies corresponding to TSAP or TSIP proteins are useful for diagnostic purposes, especially for identifying a predisposition to cancer and for monitoring cancer. Cells transformed with TSAP or TSIP genes can be used to screen for anticancer and antiviral agents.

Sequence 240 BP; 68 A; 54 C; 47 G; 71 T; 0 other;

Query Match 16.2%; Score 209.2; DB 21; Length 240;
Best Local Similarity 97.9%; Pred. NO. 5.7e-28;

Matches 233; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

OY 685 atctgactgtaggtgaatgtctgagcctgctcctaataaagactcaaggaggaagtc 744
DB |||||||
OY 745 aattgggcatctgctaataagaatgaactcatgatggaacttcagttcatttctgtc 804
DB |||||||
OY 62 aattgggcatctgctaataagaatgaactcatgatggaacttcagttcatttctgt- 120
OY 805 cctgaaattccctggtctgttctcatttggagcgaattggccttgggaaaccacagt 864
DB |||||||
OY 121 cctgaaattccctggtctgttctcatttggagcgaattggccttgggaaaccacagt 180
OY 865 tcttcttccgattcttcacgtctacggtctatgcaattcctcccaatataga 922
DB |||||||
OY 181 tcttcttccgattcttcacgtctacggtctac-gctatgcaattcctcccaataaata 237

RESULT 2

AA116088
ID AAT16088 standard; cDNA; 486 BP.

XX NC AAT16088;

XX DT 30-MAY-1996 (first entry)

XX DE Mouse epimorphin fragment (23).

KW Epimorphin; human; mouse; wound; burn; epithelial tissue;
KW diagnosis; treatment; morphogenetic abnormality; cosmetic;
KW hair growth stimulator; ds.

XX OS Mus musculus.

XX PN EP698666-A2.

XX PD 28-FEB-1996.

XX PF 20-JUN-1995; 95EP-0304270.

XX PR 31-MAR-1995; 95JP-0099980.

XX PR 21-JUN-1994; 94JP-0162874.

XX PR 31-MAR-1995; 95JP-0099979.

XX PA (SUME) SUMITOMO ELECTRIC IND CO.

XX PI Hiral Y, Koshida S, Oka Y;

XX

DR WPI: 1996-118213/13.

DR P-FSDB; AAR92048.

XX Novel polypeptide containing an epimorphin functional domain - has possible benefits in epithelial tissue treatments, e.g. burns and for artificial organs

PS Claim 27; Page 32; 62pp; English.

XX New polypeptides contain a first portion of 5-99 amino acids joined to a second portion contg. at least a functional domain of epimorphin. The first portion may be selected from the peptides given in AAR92029 to AAR92036. The second portion may be full-length epimorphin (see AAR92037 to AAR92042 for human and mouse epimorphins). Fragments (123), (2M), (3M) and (23) of epimorphin given in AAT16083 to AAT16090 are used in the prodn. of modified epimorphins.

CC 123: N-terminus to right before C-terminal hydrophobic domain.

CC 2M: amino acid 30 to right before C-terminal hydrophobic domain.

CC 3M: amino acid 79 to right before C-terminal hydrophobic domain.

CC 23: amino acid 105 to right before C-terminal hydrophobic domain.

CC The modified epimorphins are useful for the development of diagnosis

CC and treatment of morphogenetic abnormalities of epithelial tissue or

CC novel remedies for wounds, eg burns, after surgery and for artificial

CC organs. They may also be used as components of cosmetics, hair

CC growth stimulators, etc.

XX Sequence 486 BP; 152 A; 110 C; 139 G; 85 T; 0 other;

Query Match 9.6%; Score 124.8; DB 17; Length 486;

Best Local Similarity 60.7%; Pred. NO. 3.9e-13;

Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

OY 1 atccagccagctgagatcatcagggaaggagctctcggcgaccagatcaggagacatg 60
DB |||||||
OY 133 atccagccagctgagatcactggaggaccacactgacgagctggaagagatg 192
OY 61 ttcgagcagggttaagtggagcgtgtttccgagaacttctgcccagctggaaggcgcg 120
DB |||||||
OY 193 ctggagagcgggaagccgtccatcttcctcgatattatcatgattcacaatcact 252
OY 121 cgggcgcctcacaagagatgagagccgaccgcaactctgcctcggagagccgc 180
DB |||||||
OY 253 aggcagctctcaatgagatgagctcccgccacaagacatcatgaagtggagaccagc 312
OY 181 atccgagcgtacacgagctctcttcgagatgcgggtgctgtgtgagaagagccgcac 240
DB |||||||
OY 313 atccgagagctgcacgagatgttcattggtatggccatgttctcgcgagactcagggtgaa 372
OY 241 accctgaacgtcatcagctcaacgtacaaaagacggtcgcactcacccgcccaggcccaag 300
DB |||||||
OY 373 atggtcaacaacatcgagagaaatgtgtgaactctgtagattacgtggaacatgcccaag 432
OY 301 gcgcaggtgcggaagccgctgcagtcacgagagagaag 336
DB |||||||
OY 433 gaagagcagaagaagccatcaataaccagagcaag 468

RESULT 3

AA162413

ID AAT62413 standard; cDNA; 486 BP.

XX AC AAT62413;

XX DT 02-JUL-1997 (first entry)

XX Mouse epimorphin truncated variant 23 coding sequence.

KW Human; mouse; epimorphin; coiled-coil region; functional domain; tissue;
KW hydrophobic; deletion; truncation; regulation; morphogenesis; epithelium;
KW artificial organ; cosmetic; hair tonic; ds.

XX OS Synthetic.

Qy 301 ggcaggtgcgaagccgtgcagtcagtcagagagaag 336
 Db 433 GAAGAGACGAAGAAGCCATCAATAATACGAGCAAG 468

RESULT 12
 AR111443
 LOCUS AR111443 564 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 12 from patent US 6127149.
 ACCESSION AR111443
 VERSION AR111443.1 GI:12828291
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unidentified.
 REFERENCE 1 (bases 1 to 564)
 AUTHORS Hirai,Y., Koshida,S. and Oka,Y.
 TITLE Modified epimorphin
 JRNAL Patent: US 6127149-A 12 OCT-2000;
 FEATURES Location/Qualifiers
 source 1..564
 BASE COUNT 181 a 124 c 162 g 97 t
 ORIGIN

Query Match 9.6%; Score 124.8; DB 6; Length 564;
 Best Local Similarity 60.7%; Pred. No. 4e-10;
 Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 1 atccagcgcagctggagatcatggcgaaggaagtcctggcgccagcatcgagagacatg 60
 Db 211 ATCCAGCGCCAGCTGGAGATCACTGGGAGGACCACCAGCTGAGCAGGCTGGAAGATG 270

Qy 61 ttcagcagggtaagtggagcgtgtttccagagaacttgcctggcgacgtgaaggcgcg 120
 Db 271 CTGAGAGCGGGAAGCCGTCATCTTCATCTCGGATATTATATCAGATTCAAAATCACT 330

Qy 121 cggcgccctcaacagatcgagagccgaccgcaactgctgcctgagagccgc 180
 Db 331 AGGCAAGCTCTCAATGATCGATCGATCCGCCCAAGACATCATGAAGCTGGAGACCAGC 390

Qy 181 atccgcagctacacagctcttcttcagatggcggtgctggtggagaagcagccgac 240
 Db 391 ATCCGAGAGCTGCACGAGATCTTCATGGATATGCCATGTTTGTGCGAGACTCAGGTTGAA 450

Qy 241 accctgaactcagcagctcaacgtacaaaagacggtcgcactacacgcccagggcaag 300
 Db 451 ATGCTCAACAACATCGAGAGAAATGTGTGAACCTCTGTAGATTACGTGGAACATGCCAAG 510

Qy 301 ggcaggtgcgaagccgtgcagtcagtcagagagaag 336
 Db 511 GAAGAGACGAAGAAGCCATCAATAATACGAGCAAG 546

RESULT 13
 E12727
 LOCUS E12727 564 bp DNA linear PAT 24-JUN-1998
 DEFINITION DNA encoding mouse Epimorphin-derived peptide.
 ACCESSION E12727
 VERSION E12727.1 GI:3251559
 KEYWORDS JP 1997065885-A/6.
 SOURCE unidentified.
 ORGANISM Unidentified.
 REFERENCE 1 (bases 1 to 564)
 AUTHORS Koshida,S., Oka,Y. and Hirai,Y..
 TITLE TAILORED DERIVATIVE OF EPIMORPHIN
 JOURNAL Patent: JP 1997065885-A 6 11-MAR-1997;
 COMMENT SUMITOMO ELECTRIC IND LTD
 OS None
 CC Artificial sequences.

PN JP 1997065885-A/6
 PD 11-MAR-1997
 PF 29-MAR-1996 JP 1996099684
 PR 31-MAR-1995 JP 95P 99980, 19-JUN-1995 JP 95P 175540 PI
 KOSHIDA SHOGO, OKA YUMIKO, HIRAI YOHEI
 PC C12N15/09, C07H21/04, C07K7/06, C07K14/485, PC
 C12P21/02//A61K38/00,
 PC (C12P21/02,C12R1:19);
 CC strandedness: Double;
 CC topology: Linear;
 FH key Location/Qualifiers
 FH source 1..564
 FT /organism='Artificial sequences' FT
 mat_peptide 1..561
 FT /product='Epimorphin fragment designated FT
 (3M)'/notes='fragment (3M) is derived 79-265 aa of
 mouse
 Epimorphin'.
 FT Location/Qualifiers
 source 1..564
 /organism='unidentified'
 /db_xref='taxon:32644'
 BASE COUNT 181 a 124 c 162 g 97 t
 ORIGIN

Query Match 9.6%; Score 124.8; DB 6; Length 564;
 Best Local Similarity 60.7%; Pred. No. 4e-10;
 Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 1 atccagcgcagctggagatcatggcgaaggaagtcctggcgccagcatcgagagacatg 60
 Db 211 ATCCAGCGCCAGCTGGAGATCACTGGGAGGACCACCAGCTGAGCAGGCTGGAAGATG 270

Qy 61 ttcagcagggtaagtggagcgtgtttccagagaacttgcctggcgacgtgaaggcgcg 120
 Db 271 CTGAGAGCGGGAAGCCGTCATCTTCATCTCGGATATTATATCAGATTCAAAATCACT 330

Qy 121 cggcgccctcaacagatcgagagccgaccgcaactgctgcctgagagccgc 180
 Db 331 AGGCAAGCTCTCAATGATCGATCGATCCGCCCAAGACATCATGAAGCTGGAGACCAGC 390

Qy 181 atccgcagctacacagctcttcttcagatggcggtgctggtggagaagcagccgac 240
 Db 391 ATCCGAGAGCTGCACGAGATCTTCATGGATATGCCATGTTTGTGCGAGACTCAGGTTGAA 450

Qy 241 accctgaactcagcagctcaacgtacaaaagacggtcgcactacacgcccagggcaag 300
 Db 451 ATGCTCAACAACATCGAGAGAAATGTGTGAACCTCTGTAGATTACGTGGAACATGCCAAG 510

Qy 301 ggcaggtgcgaagccgtgcagtcagtcagagagaag 336
 Db 511 GAAGAGACGAAGAAGCCATCAATAATACGAGCAAG 546

RESULT 14
 AR111442
 LOCUS AR111442 711 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 11 from patent US 6127149.
 ACCESSION AR111442
 VERSION AR111442.1 GI:12828290
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unidentified.
 REFERENCE 1 (bases 1 to 711)
 AUTHORS Hirai,Y., Koshida,S. and Oka,Y.
 TITLE Modified epimorphin
 JOURNAL Patent: US 6127149-A 11 OCT-2000;
 FEATURES Location/Qualifiers
 source 1..711

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polyA_site 229
BASE COUNT 68 a 54 c 47 g 71 t
ORIGIN
Query Match 16.2%; Score 209.2; DB 9; Length 240;
Best Local Similarity 97.9%; Pred. No. 2.5e-23;
Matches 233; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
QY 685 atctgacttaggggaatgtctgagcctgctcctctaataagactcaaggaggagtc 744
Db 2 ATCTGACTAGGGGTAAGTGTCTGAGCCTGCTCCTTAATAAGACTCAAGGAGGAGTC 61
QY 745 aattggcctcgtctaataagaactcatgatgaaacttcagttcatttactttgtc 804
Db 62 AATTGGGCATCTGTAATAGACTCATGATGGAACCTTCAGTTCAATTACTTTGT- 120
QY 805 cctgaattcctcgttctgttccattttgagcgaattggccttgggaaacaccagt 864
121 CCTGAAATTCCTGGTCTGTTCTCCATTTGAGCGAAATGGCTTGGGAAAAACCCAGT 180
QY 865 tcttcttccgattctcattcgcgttctacgctgatgcaattcctccccaatataga 922
Db 181 TCTTCTCTCCGATCTTCATCCGGTCTAC-GCTATGCAATTCCTCCCAAAAAA 237

RESULT 8
LOCUS G32623 156 bp DNA linear STS 24-SEP-1999
DEFINITION A009K37 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G32623
VERSION G32623.1 GI:5923144
KEYWORDS STS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 156)
AUTHORS Adams,M.D.
TITLE Human STS sequences
JOURNAL Unpublished
COMMENT
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Email: mdadams@tigr.org
Primer A: CATACATGTCATATGTAATCA
Primer B: CGGCTATATTTGGGTATTT
STS size: 156
PCR Profile:
Denaturation: 96C 5min
Anneal: 54C 30sec
Extend: 72C 30sec
Denature: 95C 30sec
FinalExtend: 72C 5min
Cycles: 30
Protocol:
GenomicDNA: 25 ng
Primer: 0.43 uM each
dNTPs: 230 uM each
Amplify: 0.5 units
TagStart Ab: 0.5 units
Total Volume: 10 ul
Buffer:
Tris-HCl pH8.8: 100 mM
KCl: 500 mM
MgCl2: 20 mM
Triton X-100: 1%
Concentration: 10X
Prepared with primer pairs derived from THCL20341: GenBank
Accession Numbers- R65594, R33852, T25062, L70341.
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/db_xref="taxon:9606"
/clone_lib="Human"
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primer_bind complement(134..156) 48 t
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ORIGIN
Query Match 10.5%; Score 135.6; DB 11; Length 156;
Best Local Similarity 94.0%; Pred. No. 6.9e-12;
Matches 141; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1017 tatatttggtattattttccaaacatttttaagcactgaatatcgaaacactcaa 1076
Db 150 TATTTTGGGTATTATTTTCCCAACATTTTAAAGCACTGAATATGCAACGACTCAA 91
QY 1077 attgaagtacgtcatgtttgtgtatttttcgctgataaaaaattatttaacattata 1136
Db 90 ATTGAAGTATCATGTATGTTTGTGTTATTTTCGCTGATAAAAAATTATTTAACATTATA 31
QY 1137 ttttacttgattacatgacatgcatg 1166
Db 30 TTTTACTTGATTACATATGCACATGTATG 1

RESULT 9
LOCUS RATSNTX2B 825 bp mRNA linear ROD 26-OCT-1993
DEFINITION Rattus norvegicus syntaxin 2, mRNA, complete cds.
ACCESSION L20888
VERSION L20888.1 GI:349314
KEYWORDS syntaxin 2; vesicular transport receptor.
SOURCE Rattus norvegicus (library: lambda Zap II) cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 825)
AUTHORS Bennett,M.K., Garcia-Ararras,J.E., Elferink,L.A., Peterson,K.,
Fleming,A.M., Hazuka,C.D. and Scheller,R.H.
TITLE The syntaxin family of vesicular transport receptors
JOURNAL Cell 74 (5), 863-873 (1993)
MEDLINE 93386759
FEATURES
Location/Qualifiers
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/tissue_lib="lambda Zap II"
1..825
/note="syntaxin 2, differs from syntaxin 2 and 2' only at
the carboxyl terminal end in the transmembrane region"
/codon_start=1
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/protein_id="AAA03048.1"
/db_xref="GI:349315"

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1..825
/note="syntaxin 2, differs from syntaxin 2 and 2' only at
the carboxyl terminal end in the transmembrane region"
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BASE COUNT 252 a 187 c 242 g 144 t
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Best Local Similarity 58.4%; Pred. No. 3.4e-10;
Matches 219; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
QY 1 atccagccagctggagatcatgggcaaggagtctcggcgaccagatcgaggacatg 60
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KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 207379)
JOURNAL Hu.X. and Roe,B.A.
AUTHORS Mus musculus Chromosome 10 BAC Clone rp23-111d4
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 207379)
AUTHORS Hu.X. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2001) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT On Jan 29, 2002 this sequence version replaced gi:17861042.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR

* NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
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* 2294: contig of 2294 bp in length
* 2295: gap of unknown length
* 2395: contig of 3289 bp in length
* 5684: gap of unknown length
* 5684: gap of unknown length
* 5784: contig of 2846 bp in length
* 8629: gap of unknown length
* 8630: contig of 3628 bp in length
* 8729: gap of unknown length
* 12357: gap of unknown length
* 12458: contig of 4230 bp in length
* 16688: gap of unknown length
* 16787: gap of unknown length
* 16788: contig of 3226 bp in length
* 20013: gap of unknown length
* 20114: contig of 4149 bp in length
* 24262: gap of unknown length
* 24362: gap of unknown length
* 24363: contig of 3338 bp in length
* 27001: gap of unknown length
* 27801: contig of 4025 bp in length
* 31826: gap of unknown length
* 31926: contig of 5889 bp in length
* 37915: gap of unknown length
* 37915: contig of 5645 bp in length
* 43560: gap of unknown length
* 43660: contig of 6104 bp in length
* 49664: gap of unknown length
* 49864: contig of 5307 bp in length
* 55171: gap of unknown length
* 55271: contig of 4302 bp in length
* 59573: gap of unknown length
* 59673: contig of 5607 bp in length
* 65379: gap of unknown length
* 65380: contig of 5232 bp in length
* 70612: gap of unknown length
* 70712: contig of 5610 bp in length
* 76322: gap of unknown length
* 76422: contig of 10407 bp in length
* 86829: gap of unknown length
* 86929: contig of 7494 bp in length
* 94423: gap of unknown length
* 94522: contig of 7796 bp in length
* 102319: gap of unknown length
* 102419: contig of 8521 bp in length
* 110939: gap of unknown length
* 110940: contig of 8879 bp in length
* 11918: gap of unknown length
* 11919: gap of unknown length

* 120019 130825: contig of 10807 bp in length
* 130826 130925: gap of unknown length
* 130926 140713: contig of 9788 bp in length
* 140714 140813: gap of unknown length
* 140814 152889: contig of 12076 bp in length
* 152890 152989: gap of unknown length
* 152990 164750: contig of 11761 bp in length
* 164751 164850: gap of unknown length
* 164851 177836: contig of 12986 bp in length
* 177837 177936: gap of unknown length
* 177937 191981: contig of 14045 bp in length
* 191982 192081: gap of unknown length
* 192082 207379: contig of 15298 bp in length.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="10"
/clone="rp23-111d4"
/clone_lib="RPCI mouse BAC library 23"
BASE COUNT 57773 a 45400 c 44678 g 56655 t 2873 others
ORIGIN
Query Match 30.7%; Score 397.2; DB 2; Length 207379;
Best Local Similarity 65.5%; Pred. No. 3.6e-52;
Matches 833; Conservative 0; Mismatches 383; Indels 56; Gaps 15;
QY 1 atccagcgccagctggagatcatgggcaaggagctctcggcgaccagatcgaggacatg 60
DB 91358 ATCCAGGCGCAGCTGGAGATCATGGCAAGGACATGTCGGGCGAGCAGATTGAGGACATG 91417
QY 61 ttcgagcgaggttaagtggagcgtgtttccgagaaacttctggtccgacagtgaaggcgcg 120
DB 91418 TTCGAGCAGGGCAAGTGGGATGATTCTCCGAGAACCTCTGGCCACCTTGAAGGGCGG 91477
QY 121 cggcgccgctcaacgagatcgagcgccaccgcaactgctgcgctggaagagcgcg 180
DB 91478 CGGGTGCCTCAACGAGATCGAGAGCCGCCACCGGAGCTCTGCGCTGGAGGGTGGC 91537
QY 181 atccgagctacacgagctcttcttgagatggcggtgctggtgagagcgagcgac 240
DB 91538 ATTCCGGATGTGCACGAGCTCTTCTTACAGATGGCGGTGCTAGTGAGAAGCAGGAGGAC 91597
QY 241 accctgaacgtcatcgagctcaacgtacaaaagacaggtcgactacacggcgccaggaag 300
DB 91598 ACGCTGACGTCATCGAGCTTAACGTCGAGAAGACCCCTCGATTACACGGCGAGGCCAAG 91657
QY 301 gcgaggtgcgaagcgctgagtagcagtagcagtagcagtagcagtagcagtagcagtagc 360
DB 91658 GCGCAGGTGCGCAAGCGGTGCGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 91717
QY 361 ttctgtgtccctgctcaagttagcagggcgccgcccggcgccaccccgccatcccgagacc 420
DB 91718 TTCTGTGTTCCTGTGTCAACTAGC-CGCTGGCTTTCAGTCTCCACTGCAGTGCCCA-TGT 91775
QY 421 atgagcgcgctgggaagagcgtcaccgaagccggagagctctgctccctcagggagttgcc 480
DB 91776 GGGAAACATGTCTCAGGATGCCAGCCAAAGGACCTTTGTCACCTGGGCGGAGGAGGGTC 91835
QY 481 ccaaccccttcggaactcagctcttagaaaa---gaaacgcccaggttcaagaattgcaa 537
DB 91836 CCAATACCTTGCAGAAATTCAGAGCATAGAGAAAGTGGGGTTGGGATGCAAGATTTGGAG 91895
QY 538 accagcctgtgctgaaagatggttagttgataccgctccgagattcttctcagtaagat 597
DB 91896 TCCGGCACCTGTGCCTTCAAGGAATAGTTGTTAAATATCAATGGGTACTTAATGTAGAC 91955
QY 598 agattccac-aagttgtgcaatgcatatataatgacaccttgcaactcttaccgcttga 656
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Best Local Similarity 99.7%; Pred. No. 2.2e-181;
Matches 1260; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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Qy 61 ttcgagcaggtaagtggagctgtttccgagaaacttctggtggcgacgtgaaggcgcg 120
Db 35840 TTCGAGCAGGTAAGTGGGACGTGTTTTCCGAGAACTTGTCTGGCGGACGTGAAGGGCGCG 35899

Qy 121 cgggcgcctcaacgagatcgagagcgccaccgcgaactctgcctgcctggagagcgcg 180
Db 35900 CGGGCGCCCTCAACGAGATCGAGAGCGCCACCACCGGAACCTGCTGGCGCTGGAGAGCCGC 35959

Qy 181 atccgagctacagagctcttcttcagatggcggtgctggtggagaaagcagccgac 240
Db 35960 ATCCGCGAGCTACAGAGCTCTTCTTGAGATGGCGGTGCTGGTGGAGAAGCAGCGCCGAC 36019

Qy 241 accctgaagctcatgagctcaacgtacaaaagacggtcgactacacggcgccagccaaag 300
Db 36020 ACCCTGAACGCTCATCGACTCAACGTACAAAAGACGGTCTGACTACCCGGCCAGGCCCAAG 36079

Qy 301 gcgcaggtgcgaaagcgctgcagtcacgagagaagaccctcgcgaccctctgctgc 360
Db 36080 GCGCAGGTGCGGAAGCGCGTGCAGTACCGGAGAGAACCCCTGCGGACCCCTCTGCTGC 36139

Qy 361 tctgtctccctgcctcaagtagcagcgccgcccggcgccaccgccctccagacc 420
Db 36140 TTCTGCTGCTCCTGCTCAAGTAGCAGCGCGCGCGCGCCGCGCCACGCCCATCCCGAGACC 36199

Qy 421 atgagcgctgggaagacgtcaacaaagccggagctctgctgcctcaggagattgcc 480
Db 36200 ATGGAGCGCGCTGGGAAGGAGCG-CACCAAGACCGGGAGCTCTGCCCTCAGGGAGTTGCC 36258

Qy 481 ccaaccccttcgcgaactcagctcttttagaagaacccaggttcgaagattgcaaac 540
Db 36259 CCNACCCCTTCGGNACTCAGCTCTTTAGAAAAGAAACCCAGGTTCAAGATTGCAAAACC 36318

Qy 541 agcctgtgcttggaagatggttagttgataccgctcccgatgattcttcagtaaaataga 600
Db 36319 AGCCTGTGCTTGGAAGATGTTAGTTGATACCGTCCGATGATCTTTCAGTAAAGATAGA 36378

Qy 601 ttcccaaaagtgtgcaatgtcattatataatgacacctgcactcttaccgtttgacaga 660
Db 36379 TTCCCAAAAGTTGTCAATGTCAATTATATGACACTTGCACCTTGTACCGTCTTGACAGA 36438

Qy 661 agccaagttaagaactgaagtgtatctgactgtgaggtgaatgtctgagggcctgcctcc 720
Db 36439 AGCCAAGTTAAGAACTGAAGTTGATCTGACTGTAGGGTGAATGTCTGAGGCGCTGCCCTCC 36498

Qy 721 taataaagactcaaggaggaagtcaattgggcatctgctgtaataagaatgaactcatgatgg 780
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Db 36559 AAACCTTCAGTTACTTTTGT-CCTGAAAATTCGCTGGTCTGTTCCTCAATTTTGAGCGA 36617
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Qy 901 gcaattctcccccataatagatcttcttctctctctctctctctctctcttataaaatcac 960
Db 36677 GCAATTTCTCCCAATATAGATCTTATTTCTGCTCATTTCCCTCTACTTATTAATCAAC 36736
Qy 961 accaaacactactatttcttctctctctctctctctctctctctctctctccacgggttata 1020
Db 36737 ACCAAACACTTACTATTTTCTTATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 36796
Qy 1021 ttttggtattttttccaaacatttttaagcactgaataatcgaacaaagcactcaaatg 1080
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Db 36917 TACTTGATTACATATGCACATGATGTAATACTGTAATACTAATAATATCTACTAATATATGT 36976
Qy 1201 acataatgacatggttggtttaactcttcttctgtaagtgatggtataataatctcaagacg 1260
Db 36977 ACATATGATCAATGCTTAACTTCTTTTGTAGTATGATATATAATAATTTCAAGACG 37036
Qy 1261 aaaa 1264
Db 37037 AACCA 37040

RESULT 3
AF044309
LOCUS Homo sapiens syntaxin 11 mRNA, complete cds. PRI 23-JUN-1998
DEFINITION AF044309
ACCESSION AF044309
VERSION AF044309.1 GI:3248917
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1280)
AUTHORS Advani,R.J., Bae,H.R., Bock,J.B., Chao,D.S., Douny,Y.C.,
Prekeris,R., Yoo,J.S. and Scheller,R.H.
TITLE Seven novel mammalian SNARE proteins localize to distinct membrane
compartments
JOURNAL J. Biol. Chem. 273 (17), 10317-10324 (1998)
MEDLINE 98221163
REFERENCE 2 (bases 1 to 1280)
AUTHORS Yoo,J.-S. and Scheller,R.H.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-1998) Molecular and Cellular Physiology, Stanford
University, Stanford, CA 94305, USA
FEATURES
source location/Qualifiers
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184..1047
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/protein_id="AAC24031.1"
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AUTHORS Amson, R.B.
TITLE Direct Submission
JOURNAL Submitted (22-OCT-1998) Amson R.B., Tumor Suppression, CEPH Human Polymorphism Study Center, 27 rue Juliet Dodu Paris, 75010, FRANCE
FEATURES Location/Qualifiers
source 1..1296
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/db_xref="taxon:9606"
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polya_signal 723..728
polya_site 1262
BASE COUNT 370 a 305 c 282 g 339 t
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Query Match 99.2%; Score 1284; DB 9; Length 1296;
Best Local Similarity 99.9%; Pred. No. 1.2e-190;
Matches 1295; Conservative 0; Mismatches 0; Indels 1; Gaps 1
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Db 1 ATCCAGCGCCAGCTGGAGATCATGGCAAGGAAGTCTCGGCGCACCATCGAGGACATG 60
QY 61 ttccagcagggttaagtgggacgtgtttcccgagaacttgctggccgacgtgaaggcg-cgc 119
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Db 61 TTCGAGCAGGGTAAGTGGGACGTGTTTCCGAGAACTTGCTGGCGACGCTGAAGGCCCG 120
QY 120 gcggcgccctcaacagatcgaagacgcgcacgcgaactgctgcctggagagccg 179
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Db 121 CGGGCGCCCTCAACAGAGATCGAGAGCGGCCACCGGAACCTGCTGCGCTGGAGAGCCG 180
QY 180 catccgcagctcacagagctcttcttcgacagtgcggtgcgtggtggtggaagcagccga 239
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Db 181 CATCGCGACGTACACGAGCTCTTCTTCGAGATGGCGGTGCTGTGTGGAGAGCAGGCCGA 240
QY 240 caccctgaacgtcatcgagctcaacgtaacaaagacggtcgactacacccgcccaggccaa 299
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Db 241 CACCCTGAACGTATPCGAGCTCAACGTCACAAAGACGGTCGACTACACCGCGCCAGGCCAA 300
QY 300 ggcgcagtgctcggaagccgtgcagtacgaggaagaacccctccggaccctctgctg 359
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Db 301 GCGCGAGGTGCGAAGGCCGTGCAGTACGAGGAAGAACCCTTCGCGGACCTCTGTCTG 360
QY 360 ctctgctgctccctgcctcaagtacgagcgccgcggccgcgcacccgccatcccgagac 419
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Db 361 CTCTGCTGTCCCTGCCTCAAGTACGAGCGCGCCCGGCGCCACCGCCCATCCCGAGAC 420
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Db 421 CATGAGCGCGCTGGGAAGGAGCTCACCAAAGCCGGAGCTGTGCCCTCGAGGGAGTTGC 480
QY 480 cccaaccttccgggaactcagctctttagaagaagaaacccaggttcaagaattgcaaac 539
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QY 720 ctaataaagactcaaggaggaagtcgaattgggcacatctgactgaataagaatgaactcatgatg 779
Db 721 CTATAAAGACTCAAGGAGGAAGTCATTTGGGCATCTGCTAATAGAAATGAATCATGATG 780
QY 780 gaaacttcagttcatttacttctgtccctgaaaaattccctgggttctggttccatttggagcg 839

